CLAIMS

1. (Currently Amended) A method of obtaining information about a chemically active area of a target molecule, comprising:

providing a set of substantially rigid chemical gauges, each of said gauges providing at least one substantially rigid triangular geometric substructure of binding points, such that at least 50% of a mathematical-chemical space is spanned by the substantially rigid triangular geometric substructures of said gauges, each point in said space being covered by at least 5 distinct gauges from said set;

said mathematical-chemical space being defined using a list of at least six chemical binding point types, including acid, base, hydrophobic, hydrogen-bond donor, hydrogen-bond acceptor, aromatic, and a range of possible distances between chemical binding points including the range of 2-12 angstrom, said list and said range defining a space of possible triangular configurations, each configuration including a triplet of distances within said range that form a triangle and a triplet of binding types for the triangle vertices; and

a portion of said space being defined as being spanned if there is at least one substantially rigid triangular substructure available to chemically bind to a triangular configuration of binding points selected in said portion,

causing said target to interact with a plurality of gauges of said set of gauges;

assaying said interaction of said gauges with said target to obtain a plurality of assay results; and

analyzing said assay results to obtain information about said chemically active area.

2. (Currently Amended) A method according to claim 1, wherein said space includes a portion covering the range of between 4 and 8 angstrom, said portion spanned at least 50%. ~~wherein said gauges allow rotation of moieties of said gauges.~~

3. (Original) A method according to claim 1, wherein said gauges are constructed using a rigid scaffold.

4. (Original) A method according to claim 1, wherein constituent atoms of said gauges do not move more than 1 Å unless at least 20Kcal/Mol are applied to the gauge.

5. (Original) A method according to claim 1, wherein analyzing comprises identifying a plurality of spatial and chemically specific bindings configurations in said target active area.

6. (Original) A method according to claim 5, wherein said configurations comprise triangular configurations.

7. (Withdrawn) A method according to claim 5, wherein identifying comprises identifying a configuration that matches a configuration of a bound gauge.

8. (Withdrawn) A method according to claim 5, wherein identifying comprises identifying a configuration that does not match a configuration of a bound gauge.

9. (Original) A method according to claim 8, wherein identifying comprises identifying by statistical analysis of said assay results.

10. (Withdrawn) A method according to claim 9, wherein identifying comprises identifying by clustering.

11. (Withdrawn) A method according to claim 5, wherein identifying comprises assuming each gauge indicates a single configuration.

12. (Withdrawn) A method according to claim 5, wherein identifying comprises assuming at least some of the gauges indicate a plurality of configurations.

13. (Withdrawn) A method according to claim 5, wherein identifying comprises classifying gauges by chemical moieties at vertexes of said configurations.

14. (Original) A method according to claim 1, comprising reconstructing a spatial map of at least part of said chemically active area, from at least two of said assay results, said part including at least four chemical binding areas.

15. (Original) A method according to claim 14, wherein said part includes at least six chemical binding areas.

16. (Original) A method according to claim 5, comprising reconstructing a spatial map of at least part of said chemically active area, from at least two of configurations, said part including at least four chemical binding points.

17. (Original) A method according to claim 16, wherein said part includes at least six chemical binding areas.

18. (Original) A method according to claim 16, wherein reconstructing comprises:
test-reconstructing a plurality of spatial maps from said configurations;
scoring said maps; and
selected a spatial map based on its score.

19. (Withdrawn) A method according to claim 16, wherein reconstructing comprises:
test-reconstructing a plurality of spatial maps from said configurations;
clustering said maps according to common substructures; and
selected a spatial map based on a relative property of a cluster it belongs to.

20. (Original) A method according to claim 19, wherein said relative property comprises size.

21. (Original) A method according to claim 16, wherein said spatial map includes enough binding points to ensure binding of a small molecule drug having a chemical profile matching the binding points.

22. (Original) A method according to claim 21, wherein said spatial map includes at least 6 binding points.

23. (Original) A method according to claim 21, wherein said spatial map includes at least 8 binding points.

24. (Original) A method according to claim 1, wherein said set of gauges comprises a set of gauges with at least 10,000 gauges.

25. (Original) A method according to claim 1, wherein said set of gauges comprises a set of gauges with at least 50,000 gauges.

26. (Original) A method according to claim 1, wherein said gauges comprise moieties arranged in spatial configurations and wherein said gauges are selected to span a virtual space of spatial chemical configurations.

27. (Original) A method according to claim 1, wherein substantially each point of virtual space that is spanned by said gauges is covered by at least two gauges.

28. (Original) A method according to claim 1, wherein substantially each point of virtual space that is spanned by said gauges is covered by at least three gauges.

29. (Original) A method according to claim 1, wherein at least 0.5% of said gauges bind with said target.

30. (Original) A method according to claim 1, wherein at least 1% of said gauges bind with said target.

31. (Original) A method according to claim 1, wherein at least 3% of said gauges bind with said target.

32. (Original) A method according to claim 1, wherein at least 50% of said gauges are defined by adding moieties to a set of fewer than 100 scaffolds.

33. (Original) A method according to claim 1, wherein at least 50% of said gauges are defined by adding moieties to a set of fewer than 50 scaffolds.

34. (Original) A method according to claim 1, wherein at least said set of gauges uses fewer than 15 different chemical moieties to define the chemical behavior of said gauges.

35. (Original) A method according to claim 1, wherein at least said set of gauges uses fewer than 10 different chemical moieties to define the chemical behavior of said gauges.

36. (Original) A method according to claim 1, wherein said assay is a functional assay.

37. (Withdrawn) A method according to claim 1, wherein said assay is a binding assay.

38. (Withdrawn) A method according to claim 1, wherein said assay is a cellular assay.

39. (Withdrawn) A method according to claim 1, wherein said assay is a flow-through assay.

40. (Original) A method according to claim 36, wherein said functional assay is performed in the presence of a natural substrate of said target.

41. (Original) A method according to claim 1, wherein said target comprises a protein including a biochemically active area adapted to engage a substrate.

42. (Original) A method according to claim 41, wherein said chemically active area comprises an area including said biochemically active area.

43. (Original) A method according to claim 41, wherein said chemically active area comprises a control area of said protein.

44. (Original) A method according to claim 1, analyzing comprises analyzing successful binding of at least 60 gauges.

45. (Original) A method according to claim 1, analyzing comprises analyzing successful binding of at least 10 gauges.

46. (Original) A method according to claim 1, analyzing comprises analyzing successful binding of at least 100 gauges.

47. (Original) A method according to claim 5, wherein identifying comprises identifying at least 40 different configurations.

48. (Original) A method according to claim 5, wherein identifying comprises identifying at least 10 different configurations.

49. (Original) A method according to claim 5, wherein identifying comprises identifying at least 100 different configurations.

50. (Original) A method according to claim 16, comprising:

comparing said map to a lead data base; and

selecting a lead from said data base for further use responsive to a semblance or lack of semblance between said lead and said map.

51. (Original) A method according to claim 16, comprising:

comparing said map to a lead data base; and

rejecting a lead from said data base for further use responsive to a semblance between said lead and said map.

52. (Original) A method according to claim 16, comprising:

constructing a lead to have a semblance to said map.

53. (Original) A method according to claim 52, wherein constructing comprises constructing using said gauges or scaffolds used to define said gauges.

54. (Original) A method according to claim 5, comprising:

comparing said configurations to a lead data base; and

selecting a lead from said data base for further use responsive to a matching of said configurations to said lead.

55. (Original) A method according to claim 5, comprising:

constructing a lead based on said configurations.

56. (Original) A method according to claim 5, comprising:
selecting at least one of said gauges as a lead for drug discovery.

57. (Original) A method according to claim 1, comprising comparing the binding of gauges with similar binding geometries to obtain steric clashing data; and
analyzing said steric clashing data to provide geometrical information about said target.

58. – 101. (Cancelled)

102. (Original) A method according to claim 1, comprising generating a set of drug leads for said target based on said information.

103. (Original) A method according to claim 102, comprising removing known drug leads for said target from said set.

104. – 154. (Cancelled)

155. (Previously presented) A method according to claim 1, wherein said analyzing comprises characterizing said chemically active area.

156. (Previously presented) A method according to claim 155, wherein said chemically active area comprises at least two disjoint chemically active areas.

157. (Previously presented) A method according to claim 1, wherein said analyzing comprises taking said rigidity into account of said analyzing.

158. (Previously presented) A method according to claim 1, wherein said target molecule comprises an agricultural chemical target.

159. (Previously presented) A method according to claim 1, wherein said target molecule comprise a drug target.

160. (Previously presented) A method according to claim 1, wherein, on the average, each point of virtual space that is spanned by said gauges is covered by between 1.1 and 2 gauges.

161. (Previously presented) A method according to claim 1, wherein at least 0.1% of said gauges bind with said target.

162. (Previously presented) A method according to claim 1, wherein the moieties comprise Hydroxyl (OH), Carboxyl (COOH), Amide (CONH2), Ethyl (CH2-CH3), Propyl (CH2-CH2-CH3), Phenyl (C6H5, 6 member aromatic ring).

163. (Previously presented) A method according to claim 1, wherein said chemically active area comprises at least two disjoint chemically active areas.

164. (Previously presented) A method of mapping an active area of a biological target, comprising:

providing a set of chemical gauge molecules, each gauge molecule having a geometric structure;

assaying an interaction between a plurality of said chemical gauge molecules and the biological target; and

mapping the active area according to the results of assaying said interactions and according to said gauge molecule geometric structures.

165. (Previously presented) A method according to claim 164, wherein said gauge molecules are rigid molecules.

166. (Previously presented) A method according to claim 164, in which the gauge molecules are composed of a rigid scaffold and to which various chemical moieties are attached using one rotationally free bond.

167. (Previously presented) A method according to claim 166, wherein the rigid scaffold containing no rotationally free bonds.

168. (New) A method according to any of claims 1, wherein said spanning covers at least 50% of points in said space that include a acid.

169. (New) A method according to claim 1, wherein said space includes a portion covering the range of between 4 and 12 angstrom, said portion spanned at least 50%.

170. (New) A method according to claim 1, wherein said space includes a portion covering the range of between 8 and 12 angstrom, said portion spanned at least 50%.

171. (New) A method according to claim 1, wherein said potential scaffold is judged rigid if it is rotationally rigid.